

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 31, 2003, 13:11:02 ; Search time 25 Seconds
(without alignments)
989.442 Million cell updates/sec

Title: US-10-082-894-2

Perfect score: 2786

Sequence: 1 MDKYQNVQKQVCLVIDWG.....LMGLPVPPEMDGVPLLEQRG 526

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries.

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1153.5	41.4	515	1	GM11_METAC
2	1151.5	41.3	512	1	GM11_CLOPE
3	1143.5	41.0	510	1	GM11_LISIN
4	1143.5	41.0	521	1	GM12_METAC
5	1141.5	41.0	510	1	GM11_LISMO
6	1127	40.5	510	1	GM11_BACST
7	1124.5	40.4	521	1	GM11_METWA
8	1120	40.2	510	1	GM11_BACHD
9	1118	40.1	510	1	GM11_BACSU
10	1103.5	39.6	511	1	GM11_BACME
11	1088.5	39.1	515	1	GM11_PSEAE
12	1083.5	38.9	510	1	GM11_VIBCH
13	1082	38.8	514	1	GM11_SALTI
14	1078	38.7	533	1	GM11_ANASP
15	1076	38.6	514	1	GM11_SALTY
16	1073.5	38.5	515	1	GM11_YERPE
17	1070.5	38.4	512	1	GM11_OCEIH
18	1067.5	38.3	514	1	GM11_SHEON
19	1065	38.2	510	1	GM11_CLOAB
20	1063	38.2	514	1	GM11_ECOLI
21	1059	38.0	514	1	GM11_ECO57
22	1057	37.9	510	1	GM11_SHIFL
23	1055	37.9	510	1	GM11_PSESM
24	1044.5	37.5	531	1	GM11_SYNEL
25	1023	36.7	508	1	GM11_MYCPN
26	1023	36.7	532	1	GM11_SYNT3
27	999.5	35.9	505	1	GM11_AGRTP5
28	996	35.8	491	1	GM11_HELPY
29	991	35.6	491	1	GM11_HELPJ
30	990.5	35.6	534	1	GM11_PORPU
31	975	35.0	505	1	GM11_STAAM
32	970	34.8	505	1	GM11_STAAN
33	967.5	34.7	508	1	GM11_HALNI

ALIGNMENTS

RESULT 1

ID	GM11_METAC	STANDARD;	PRT;	515 AA.
AC	Q8TWI6:			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	2,3-bisphosphoglycerate-independent phosphoglycerate mutase 1			
DE	(EC 5.4.2.1) (Phosphoglyceromutase 1) (BPG-independent PGAM 1)			
DE	(iPGM 1).			
GN	GMPI1 OR WA2671.			
OS	Methanosarcina acetivorans.			
OC	Archaea; Euryarchaeota; Euryarchaeota orders Incertae sedis;			
OC	Methanosarcinales; Methanosarcinaceae; Methanosarcina.			
OX	NCBI_TaxID=2214;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C2A / ATCC 35395 / DSM 2834;			
RX	MEDLINE=21929760; PubMed=11932238;			
RA	Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,			
RA	FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,			
RA	Allen N., Naylor J., Stange-Thomann N., DeAtellano K., Johnson R.,			
RA	Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,			
RA	Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,			
RA	Hedderich R., Ingram-Smith C., Kuettnar H.C., Krzycki J.A.,			
RA	Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,			
RA	Springer T.A., Unayam L.A., White O., White R.H., de Macario E.C.,			
RA	Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,			
RA	Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,			
RA	Metcalfe W.W., Birren B.;			
RT	"The genome of Methanosarcina acetivorans reveals extensive metabolic			
RT	and physiological diversity.";			
RL	Genome Res. 12:532-542(2002).			
CC	1- FUNCTION: Catalyzes the interconversion of 2-phosphoglycerate and			
CC	3-phosphoglycerate. (By similarity).			
CC	1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate -> 3-phospho-D-glycerate.			
CC	1- COFACTOR: Binds 2 manganese ions (By similarity).			
CC	1- PATHWAY: Glycolysis.			
CC	1- SIMILARITY: BELONGS TO THE BPG-INDEPENDENT PHOSPHOGLYCERATE MUTASE			
CC	FAMILY.			
CC	-----			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announcement/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
CC	EMBL; AE010963; AAM05049.1; -			
DR	HMAP; MF 01038; -; 1.			
DR	InterPro; IPR006124; Metalloenzyme.			
DR	InterPro; IPR005995; Pgm_bpd_ind.			
DR	Pfam; PF01676; Metalloenzyme; 1.			
DR	ProDom; PD004429; Pgm_bpd_ind; 1.			
DR	TIGRFAMs; TIGR01307; pgm_bpd_ind; 1.			

Db 417 AVDECLGKADKVLKEGTFTITADHGNAEVIMIDYTGKPMHTARTSDVPFLWVSKDAEG 476
Qy 481 KSTPPTGDDGKERARALRDVAPTVQLMGLPVPPEMDGVPLLEQ 524
Db 477 KSLK---DGK-----LADIAPMLVJMGLEVPSEMTGTCLLNK 512

RESULT 3
ID GPMLISIN STANDARD; PRT; 510 AA.
AC Q92812; 2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 2,3-bisphosphoglycerate-independent phosphoglycerate mutase
DE (EC 5.4.2.1) (Phosphoglyceromutase) (BPG-independent PGAM) (1PCM).
GN GPML OR PGM OR LINP550.
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1642;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CLIP 11262 / Serovar 6a;
RA MEDLINE=21537279; PubMed=11679669;
RA Glaser P., Franguel L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Krefit J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maitounam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluster T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.,
RA "Comparative genomics of *Listeria* species";
RL Science 294:849-852(2001).
CC -1- FUNCTION: Catalyzes the interconversion of 2-phosphoglycerate and
CC 3-phosphoglycerate (By similarity).
CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = 3-phospho-D-glycerate.
CC -1- COFACTOR: Binds 2 manganese ions (By similarity).
CC -1- PATHWAY: Glycolysis.
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: BELONGS TO THE BPG-INDEPENDENT PHOSPHOGLYCERATE MUTASE
CC FAMILY.
CC
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CC
CC EMBL; AL596172; CAC97777.1; -
CC PIR; A11750; A11750.
CC ListList; LIN02550; -
CC HANAP; MF_01038; -; 1.
CC InterPro; IPR006124; Metalloenzyme.
CC InterPro; IPR005995; Pgm_bpd_ind.
CC Pfam; PF01676; Metalloenzyme; 1.
CC ProDom; PD004429; Pgm_bpd_ind; 1.
CC TIGRFAMs; TIGR01307; Pgm_bpd_ind; 1.
CC Isomerase; Glycolysis; Metal-binding; Manganese; Complete proteome.
FT ACT_SITE 62 62
FT PHOSPHOSERINE INTERMEDIATE
FT (BY SIMILARITY).
FT METAL 12 12
FT MANGANESE 2 (BY SIMILARITY).
FT METAL 62 62
FT MANGANESE 2 (BY SIMILARITY).
FT METAL 402 402
FT MANGANESE 1 (BY SIMILARITY).
FT METAL 406 406
FT MANGANESE 1 (BY SIMILARITY).
FT METAL 443 443
FT MANGANESE 2 (BY SIMILARITY).
FT METAL 444 444
FT MANGANESE 2 (BY SIMILARITY).
FT METAL 461 461
FT MANGANESE 1 (BY SIMILARITY).

SQ SEQUENCE 510 AA; 56138 MW; E5AA15A804B16A4D CRC64;
Query Match 41.0%; Score 1143.5; DB 1; Length 510;
Best Local Similarity 44.2%; Pred. No. 3.4e-81;
Matches 231; Conservative 91; Mismatches 174; Indels 27; Gaps 7;
Qy 11 VCLVWIDGWSLDEQHGNIAIAKAKTPIMDKLCSGNWQ-----KLEAHGLHVLGPEGLMGN 65
Db 6 VAIILDLGFGKRAETVGNVAQANKPNFDY---WANFPHGLKAAAGLDVGLPEGQMG 61
Qy 66 SEVCHNLNIGAGRVIIYQDIVINLAVQNRNEFFVTPOIVASAEAKKSGSRHLHLGLSDGG 125
Db 62 SEVCHNLNIGAGRVIIYQSLTRIDKAIEEGEFQENKALNNAFTHTKENNSDLHLGLSDGG 121
Qy 126 VHSIDHLFALIRAFKQLQVFKVFIHFADGRDTSPTSGAGYLEQLLOFTASEKYGELAT 185
Db 122 VHSINHLVALLETAKDKGVKNVYIHFADGRDVAPOSSLEYLETLEKASLDLNYGAIAT 181
Qy 186 ITGRYAMORDKRWERIKMAYEAIVGGIGOKATVDKAVDVVVRERYAQSEDEFUKPIVFS 245
Db 182 VSGRFYAMDRKWERVEKAYKATVSAEGK--FEDPIELVKASYANDKNDKDEFVPAIT 239
Qy 246 DDGR----VKDDDTLFFNVRADRMQICECLGLERYKDLNLSVPHPKNIQISMTQYNK 301
Db 240 KDGKPVATVKNDAVIFNFRPDRAIQLSNAFTDKEDWDFDRGANHPKNIKFTMTLYNP 299
Qy 302 EFPFSLFPVPTHNTVLAELASOGVTFQFCAETEKYPHYTFPPNGGVEQFQDEECMV 361
Db 300 SDAEVAFEPIEMKNVIGEVLSNEGLSQLRIAEKYPHYTFPPNGGNEFFGENRILI 359
Qy 362 PSPKAVATYDKPEMNAAGVAEKVQIESGRHPLVMCNFAPPDMVGHTGKFEPAVKACQ 421
Db 360 NSPK-VETYDLKPMSAYEVTDAVEDIKNDKHDAIILNANPDMVGHSGMLEPTIKAE 418
Qy 422 ATDEAICKIFEACQTYNYLMVTSYDHGNAEKMAPDGESEHTAHTCNLPVPTCSKTFVFK 481
Db 419 AVDENLGRVVDLILEKGSIAIFADHGNSETMSPGKPTAHTTVPVIVTKK----- 473
Qy 482 STPTGDDGKERARALRDVAPTVQLMGLPVPPEMDGVPLLEQ 524
Db 474 -----GVTLREGGR-LADVAPTMLDLGLGVKPAEMTGESLIQK 510
RESULT 4
GM12_METAC STANDARD; PRT; 521 AA.
ID GM12_METAC
AC Q8TIY2; 2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 2,3-bisphosphoglycerate-independent phosphoglycerate mutase 2
DE (EC 5.4.2.1) (Phosphoglyceromutase 2) (BPG-independent PGAM 2)
DE (IPGM 2).
GN GP12 OR MA4007.
OS Methanobacteria acetivorans.
OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
OC Methanobacteriales; Methanobacteriales; Methanobacteriales.
OX NCBI_TaxID=2214;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=11932238;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA Fitzhugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Kuehn H.C., Krzycki J.A.,
RA Hederich R., Ingram-Smith C., Kuehn H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
RA Pritchett M., Sowers R.V., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;

RT The genome of Methanosarcina acetivorans reveals extensive metabolic
RL and physiological diversity.";
CC Genome Res. 12:532-542(2002).
CC -1- FUNCTION: Catalyzes the interconversion of 2-phosphoglycerate and
CC 3-phosphoglycerate (By similarity).
CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = 3-phospho-D-glycerate.
CC -1- COFACTOR: Binds 2 manganese ions (By similarity).
CC -1- PATHWAY: Glycolysis.
CC -1- SIMILARITY: BELONGS TO THE BPG-INDEPENDENT PHOSPHOGLYCERATE MUTASE
CC FAMILY.
CC
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CC
CC EMBL; AE011113; AM07357.1; -
DR HAMAP; MF_01038; -; 1.
DR InterPro; IPR006124; Metalloenzyme.
DR InterPro; IPR005995; Pgm_bpd_ind.
DR Pfam; PF01676; Metalloenzyme; 1.
DR ProDom; PD004429; Pgm_bpd_ind; 1.
DR TIGRFAMs; TIGR01307; Pgm_bpd_ind; 1.
KW Isomerase; Glycolysis; Metal-binding; Manganese; Complete proteome.
FT ACT_SITE 70 70 PHOSPHOSERINE INTERMEDIATE
FT METAL 20 20 (BY SIMILARITY).
FT METAL 70 70 MANGANESE 2 (BY SIMILARITY).
FT METAL 410 410 MANGANESE 1 (BY SIMILARITY).
FT METAL 414 414 MANGANESE 1 (BY SIMILARITY).
FT METAL 451 451 MANGANESE 2 (BY SIMILARITY).
FT METAL 452 452 MANGANESE 2 (BY SIMILARITY).
FT METAL 470 470 MANGANESE 1 (BY SIMILARITY).
SQ SEQUENCE 521 AA; 57685 MW; 4CF05D68DC211D93 CRC64;
Query Match 41.0%; Score 1143.5; DB 1; Length 521;
Best Local Similarity 45.8%; Pred. No. 3.5e-81;
Matches 242; Conservative 86; Mismatches 167; Indels 33; Gaps 12;
QY 8 QKVCVLVVDGSLDEQHNIAKAKTPIMDKLCSG-NQKLEAHLHVLGPEGLMGNS 66
DB 11 RRLPLMIDGVRSEASGNALAEATPLNSLLNEFPWCFLECSGEAVGLPEGMGNS 70
QY 67 EVGHLNIGAGRVYDVRINLAVORNEFTVNPQIVASAEAKKSGRSLHLLGLYSDGV 126
DB 71 EVGHLNIGAGRVYDVRINLAVORNEFTVNPQIVASAEAKKSGRSLHLLGLYSDGV 130
QY 127 HSHIDLFLALIRAFKQLOVPKVIHFFADGRDTSPTSGAGYLEQLQIFASEKYGELATI 186
DB 131 HSYMTHLYALIKLRDKGLKLVYIHAFLDGRDVPKPAALADIRELDAFCENGSAARIATV 190
QY 187 TGRYVAMDRDKWERIKMAYEAIVGIGOKATVDKAVDVVRERYAQSTDEFELKP-IVFS 245
DB 191 QGRYVAMDRDKWERIKMAYEAIVGIGOKATVDKAVDVVRERYAQSTDEFELKP-IVFS 249
QY 246 DQGR-----VKDDDTLIFNRYADRMKQICECL-----GLERYKDLNSVPHPKNIQISG 295
DB 250 SDGKEAVQDNDSTIFFNFRDRARQLTWAFENDDFGFPREK-----RPK-VHYVC 301
QY 296 MTQYNKFPFPLFPVTHTNVLAEWLASQGVTFHCAETEKYPHVTFFNNGREVOQDF 355
DB 302 MAQYDETDLPLAFPPPEELNVLGEVLSKQGLVQLRAETERYAHVTFPLNGQEKCYDG 361
QY 356 EERCWVPSKPEVATYDLPLPMNAAGVAEKWQIESGRHPLVNCNFPADWVGHGTGKEP 415
DB 362 EDRCLIPSPK-VATYDLKPEMSAYEVTDEVIRIQSGKYDVTVLNFANMDWVGHGTGIEFA 420
QY 416 AVKACQADTEATGKIFEAQCTNYVLMVTSRDNKAKM-IAPDGSSEHTAHTCNLPVFTCS 474
DB 421 AVQAEVNDVTCVGRITIEALKKAGGVALITADHGNAEQENQHTGEPHTAHTSN--PVRC- 477

QY 475 SKTEVFKSPPTGDDGKERARALRDVAPTVLQMLGVPVPEMDGVPLL 522
DB 478 --IYACKGEVKALENGK-----LSDIAPTLLDLGVKPEEMKGSLLI 518
RESULT 5
GPMI_LISMO STANDARD; PRT; 510 AA.
ID GPMI_LISMO
AC Q8Y4I4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 2.3-bisphosphoglycerate-independent phosphoglycerate mutase
DE (EC 5.4.2.1) (Phosphoglyceromutase) (BPG-independent PGAM; (IPGM).
GN GPMI OR PGM OR LMO2456.
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=EGD-e / Serovar 1/2a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaser P., Frangeul L., Buchrieser C., Rusnick C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouni F., Couve E., de Daruvar A., Deboux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kretz J., Kuhn M., Kunst F., Kurapkat G.,
RA Maudeno E., Maitoung A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehlund J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
CC -1- FUNCTION: Catalyzes the interconversion of 2-phosphoglycerate and
CC 3-phosphoglycerate (By similarity).
CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = 3-phospho-D-glycerate.
CC -1- COFACTOR: Binds 2 manganese ions (By similarity).
CC -1- PATHWAY: Glycolysis.
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: BELONGS TO THE BPG-INDEPENDENT PHOSPHOGLYCERATE MUTASE
CC FAMILY.
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CC EMBL; AL591983; CAD00534.1; -
DR PIR; AH1381; AH1381.
DR ListList; LMO2456; -
DR HAMAP; MF_01038; -; 1.
DR InterPro; IPR006124; Metalloenzyme.
DR InterPro; IPR005995; Pgm_bpd_ind.
DR Pfam; PF01676; Metalloenzyme; 1.
DR ProDom; PD004429; Pgm_bpd_ind; 1.
DR TIGRFAMs; TIGR01307; Pgm_bpd_ind; 1.
KW Isomerase; Glycolysis; Metal-binding; Manganese; Complete proteome.
FT ACT_SITE 62 62 PHOSPHOSERINE INTERMEDIATE
FT METAL 12. 12 MANGANESE 2 (BY SIMILARITY).
FT METAL 62 62 MANGANESE 2 (BY SIMILARITY).
FT METAL 402 402 MANGANESE 1 (BY SIMILARITY).
FT METAL 406 406 MANGANESE 1 (BY SIMILARITY).
FT METAL 443 443 MANGANESE 2 (BY SIMILARITY).
FT METAL 444 444 MANGANESE 2 (BY SIMILARITY).
FT METAL 461 461 MANGANESE 1 (BY SIMILARITY).
SQ SEQUENCE 510 AA; 56139 MW; 7D282159D9DFCF8 CRC64;


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Db 178 IATLSGRYSMDRDRWRKAYRAMVYGE--PTYRDLPLCIEDSKHGHIYDEFVLP 235
QY 242 IVFSDPD---VKDDDTLIFNYRADRMROICEGLGLERYKDLNASSVPKPKNIQISMT 297
Db 236 VIVREDGRPVATIONDAIIFNFPDRDRAIQISNTFTNEDFFRDRGPKPKHFLFVLIT 295
QY 298 QYNKEFPFPLSPVYTHNVLAELASQVTFHCAETEKYPHVTFFFNGGREVOFDBE 357
Db 296 HESFTKGVKAPKPTNLDNTIGEVLSQHLRLRIAEATEKYPHVTFFFNGGREKFPGED 355
QY 358 RCMVSPPEVATYDLKPMNAAGVAEKVQIESGRHPLVMCNFAPPDMVGHGKFPAPV 417
Db 356 RILINSPK-VPTYDLKPEMSAYEVDALKEIADKYDAIILNYANPDVGHSGKLEPTI 414
QY 418 KACQATDAIGKIFACQTYNVLVSDHGAERKIAPIADGSEHTAHTCNLVPTFCSSKT 477
Db 415 KAVEADEVCLGKVDAILAKGGIAITADHGNADVLDPDKPQTAHTNPNVPVIVTKG 474
QY 478 FVFKSTPTPGDGGKERARALRDVAPTIVLQMLGLPVPPMDGVPL 522
Db 475 IKLR-----DGG-----ILGLDAPTLMLDGLLPQPKMTGKSLI 508

```

RESULT 7

```

GPML_METMA
ID GPML_METMA STANDARD; PRT; 521 AA.
AC Q8PYF8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 2,3-bisphosphoglycerate-independent phosphoglycerate mutase
DE (EC 5.4.2.1) (Phosphoglyceromutase) (BPG-independent PGAM) (1PGM).
GN GPML OR MM0904.
OS Methanosarcina maezi (Methanosarcina frisia).
OC Archaea; Euryarchaeota; Euryarchaeota orders Incertae sedis;
OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2209;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Goel / Go1 / ATCC BAA-199 / DSM 3647 / OCM 88;
RX MEDLINE=2210827; PubMed=12125824;
RA Deppeiner U., Johann A., Hartsch T., Merkl R., Schmitz R.A.,
RA Martinez-Arias R., Henne A., Wlezer A., Baeumer S., Jacobi C.,
RA Brueggemann H., Lienard T., Christmann A., Boencke M., Steckel S.,
RA Bhattacharya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,
RA Fritz H.-J., Gottschalk G.;
RT "The genome of Methanosarcina maezi: evidence for lateral gene
transfer between Bacteria and Archaea.";
RL J. Mol. Microbiol. Biotechnol. 4:453-461(2002).
CC -!- FUNCTION: Catalyzes the interconversion of 2-phosphoglycerate and
CC 3-phosphoglycerate (By similarity).
CC -!- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = 3-phospho-D-glycerate.
CC -!- COFACTOR: Binds 2 manganese ions (By similarity).
CC -!- PATHWAY: Glycolysis
CC -!- SIMILARITY: BELONGS TO THE BPG-INDEPENDENT PHOSPHOGLYCERATE MUTASE
CC FAMILY.

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CC -----
CC EMBL: AF013316; AAM30600.1;
CC HAMAP: MF_01038;
CC InterPro: IPR006124; Metalloenzyme.
CC DR Pfam: PF01676; Metalloenzyme; 1.
CC DR ProDom: PD004429; Pgm_bpd_ind; 1.
CC DR TIGRFams: TIGR01307; Pgm_bpd_ind; 1.

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KW Isomerase; Glycolysis; Metal-binding; Manganese; Complete proteome.
FT ACT_SITE 70 PHOSPHOGENE INTERMEDIATE
FT METAL 20 20 MANGANESE 2 (BY SIMILARITY).
FT METAL 70 70 MANGANESE 2 (BY SIMILARITY).
FT METAL 410 410 MANGANESE 1 (BY SIMILARITY).
FT METAL 414 414 MANGANESE 2 (BY SIMILARITY).
FT METAL 451 451 MANGANESE 2 (BY SIMILARITY).
FT METAL 452 452 MANGANESE 2 (BY SIMILARITY).
FT METAL 470 470 MANGANESE 1 (BY SIMILARITY).
SQ SEQUENCE 521 AA; 57863 MW; C21EAC4898A023AA CRC64;

Query Match 40.4%; Score 1124.5; DB 1; Length 521;
Best Local Similarity 43.5%; Pred. No. 1e-79;
Matches 233; Conservative 102; Mismatches 158; Indels 43; Gaps 12;

QY 8 QOKVCLVVDGWSLDEQHGNAIAKAKTPIWDKLCSGNWK-----LEAGHLHVLGPEG 61
Db 11 RPLMLMDLGDGNGYREEKEGNAIILASTPHLDRL-----QKRPSCFLTSGEAVGLPQG 65
QY 62 LMGSEVGHNLGAGRVYIYQDIVRLINLAVQNEFVTPQIVASABRAKKGSRLLGLV 121
Db 66 QMGSEVGHNLGAGRVYIYQDIVRLINLAVQNEFVTPQIVASABRAKKGSRLLGLV 125
QY 122 SDGGVSHHDLHALIRAFKQLQVPKVIHFHFAAGRTSPTSGAGYQLQLOFTIASEYK 181
Db 126 SYGGVSHHDLHALIRAFKQLQVPKVIHFHFAAGRTSPTSGAGYQLQLOFTIASEYK 185
QY 182 ELATITGRYAMDRLKRWERTKMAEATVGGIGOKATVDKAVDVVVRERYAQSETDEFLKP 241
Db 186 KIATVQGRYAMDRLKRWERTKMAEATVGGIGOKATVDKAVDVVVRERYAQSETDEFLKP 244
QY 242 IVFSDPD---VKDDDTLIFNYRADRMROICE-----ECLGLERYKDLNASSVPKPK 290
Db 245 TIVTDSGNPEAVIQDTSIVFLNFRPDRAQLTWFVKDDDFEGFTREK-----RPF- 296
QY 291 IQISGMYNKPEFPFPLFPVTHNVLAELASQVTFHCAETEKYPHVTFFFNGGRE 350
Db 297 VHYVCMQAYDETLDLPIAFPPPELTDVLGKVLSDRGLQLRIAEATEKYPHVTFFFNGG 356
QY 351 VOFODERCMVPSPEVATYDLKPMNAAGVAEKVQIESGRHPLVMCNFAPPDMVGH 410
Db 357 KYCGEDRCLIPSPK-ISTYDLKPEMSAYEVDVVKRLISGKYDVIILNFANMDVGH 415
QY 411 GKFPAPVACATDAIGKIFACQTYNVLVSDHGAERKIAPIADGSEHTAHTCNLV 469
Db 416 GDFEAAVKAVETVDCVGRIVEALRTAGGAALITADHGNABOMENSHTEPHTAHTSN-- 473
QY 470 PFTCSSKTFVFKSTPTPGDGGKERARALRDVAPTIVLQMLGLPVPPMDGVPLLEOR 525
Db 474 PVKC---IYTCNGEVKALENGK-----LSDLAPTLLDLLEIPKPEKMTGRSLIVRK 521

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RESULT 8

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GPML_BACHD
ID GPML_BACHD STANDARD; PRT; 510 AA.
AC Q9K716;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 2,3-bisphosphoglycerate-independent phosphoglycerate mutase
DE (EC 5.4.2.1) (Phosphoglyceromutase) (BPG-independent PGAM) (1PGM).
GN GPML OR PGM OR BH3557.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058183;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;

```

RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RL halodurans and genomic sequence comparison with Bacillus subtilis.";
CC Nucleic Acids Res. 28:4317-4331(2000).
CC -!- FUNCTION: Catalyzes the interconversion of 2-phosphoglycerate and
CC 3-phosphoglycerate (By similarity).
CC -!- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = 3-phospho-D-glycerate.
CC -!- COFACTOR: Binds 2 manganese ions (By similarity).
CC -!- PATHWAY: Glycolysis.
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SIMILARITY: BELONGS TO THE BPG-INDEPENDENT PHOSPHOGLYCERATE MUTASE
CC FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AP001519; BAB07276.1; -
CC PIR; E84094; E84094.
CC HANAP; MF_01038; -; 1.
CC InterPro; IPR006124; Metalloenzyme.
CC InterPro; IPR005995; Pgm_bpd_ind.
CC Pfam; PF01676; Metalloenzyme; 1.
CC ProDom; PD004429; Pgm_bpd_ind; 1.
CC TIGRFAMs; TIGR01307; Pgm_bpd_ind; 1.
KW Isomerase; Glycolysis; Metal-binding; Manganese; Complete proteome.
FT ACT_SITE 62 62
FT METAL 12 12
FT METAL 62 62
FT METAL 403 403
FT METAL 407 407
FT METAL 444 444
FT METAL 445 445
FT METAL 462 462
SQ SEQUENCE 510 AA; 56453 MW; 52AF47C6EE03623E CRC64;
Query Match 40.2%; Score 1120; DB 1; Length 510;
Best Local Similarity 43.0%; Pred. No. 2.3e-79;
Matches 226; Conservative 98; Mismatches 174; Indels 28; Gaps 8;
QY 8 QQKVLVVIDGWSLDEOHGNAIAKAKTPIMDKLCSGNWQK-----LEAHGLHVLGPEGL 62
DB 3 KKPVALIILDFGAMRDEAKGNAVAQANKPNFDY----WNQYPHALLKADGEAVGLPEQG 58
QY 63 MGNEVGHNLGAGRVYQDQIVRLINLAVORNEFTVNPQIVASAEAKKSGRLHLLGLVS 122
DB 59 MGNEVGHNLGAGRVYQSLTRVNLNLSIREGEFFENETFLNANHVKESGLHYGLVS 118
QY 123 DGGVHSHDLHALIRAFKQLQVPKVFTHFTADGRDTSPTSGAGYLEQLLOFIASEKYE 182
DB 119 DGGHSHNLHLYALELAKRQVERVYTHGFLDGRDVGPTSAESYLVLEAKMKRELGYGE 178
QY 183 LATITGRYAMDRLKRWRIKMAVEIYGGIGQKATVDKAVDVVRYVAQSETDFLXK- 241
DB 179 LATLHGRYAMDRLKRWDRVEKSYEAMVYGE--PAYSSALVDIKDSYENSHDFVIPS 236
QY 242 IVFSDG-----RVKDDDLIFNFVRADRMROICEGLGRLYKDLNSSLVPHPKNIQISGMT 297
DB 237 VITNEDGSPVATIEDDDAIIFNFRPDRAIQMSQVFTNKDFRGDRGKLPQNYVYVCLT 296
QY 298 QYNKEFPFPLFPVTHTNVLAELASQGVTFQFCAETEKYPHYTFFFGREGVQFQDE 357
DB 297 HFSETVQGVDAFKPTNLDNTLGEVLAQQNYKQLRIATEKYPHYTFFFGSGREEFPFQEE 356
QY 358 RCMVPSPEKATYDLKPEMNAAGVAEKVVEQITSGRHRPLVMCNFAPPDMVGTGKFEPAV 417
DB 357 RILIDSPK-VATYDLKPEMSAYEYTDALLNELEADKHVILNLFANPDMMVGHSGMLEPTI 415
QY 418 KACQATDEAIGKIFEACQTYNYVLMTVSDHGNAEKMIAPDGSEHTAHTCNLVPFTCSSKT 477

Db 416 KAVEAVDECIKGVVDAILAKGGAAVITADHGNADDEVVLEGGKPMHTAHTNKVPVIVTEEG 475
QY 478 FVFVSTPTGDDGKERARALRDVAPTVLQMLGLPVPPEMDGVPLLE 523
DB 476 LNLR-----EDG-----ILADLSPTVLDDLLGGKQPAEMTKTLIK 510
RESULT 9
GPMI_BACSU STANDARD; PRT; 510 AA.
AC P39773; O32250;
DT 01-FEB-1995 (Rel. 31, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 2,3-bisphosphoglycerate-independent phosphoglycerate mutase
DE (EC 5.4.2.1) (Phosphoglyceromutase) (BPG-independent PGAM) (LPGM)
DE (Vegetative protein 107) (VEG107).
GN GPMI OR PGM.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=168 / Marburg;
RX MEDLINE=94292408; PubMed=8021172;
RA Leyva-Vazquez M.A., Setlow P.;
RT "Cloning and nucleotide sequences of the genes encoding triose
RT phosphate isomerase, phosphoglycerate mutase, and enolase from
RT Bacillus subtilis.";
RL J. Bacteriol. 176:3903-3910(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Boursier L., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Chol S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Funa S., Galizzi A., Galleron N.,
RA Ghm S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
RA Gulseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hulio M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Bianchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Mestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujić P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolan C., Rocha E., Roche B., Rose M., Sadate Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scofield F.,
RA Sekiguchi J., Sekowska A., Serró S.J., Serró P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takenaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tomonari A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler H., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.";
RL Nature 390:249-256(1997).
RN [3]
RP SEQUENCE OF 1-17.
RC STRAIN=168 / IS58;
RX MEDLINE=97443988; PubMed=9298659;
RA Antelmann H., Bernhardt J., Schmid R., Mach H., Voelker U.,
RA Hecker M.;
RT "First steps from a two-dimensional protein index towards a response-


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FT METAL 12 12 MANGANESE 2 (BY SIMILARITY).
FT METAL 62 62 MANGANESE 2 (BY SIMILARITY).
FT METAL 403 403 MANGANESE 1 (BY SIMILARITY).
FT METAL 407 407 MANGANESE 1 (BY SIMILARITY).
FT METAL 444 444 MANGANESE 2 (BY SIMILARITY).
FT METAL 445 445 MANGANESE 2 (BY SIMILARITY).
FT METAL 462 462 MANGANESE 1 (BY SIMILARITY).
FT METAL 225 225 D -> E (IN REF. 2).
SQ SEQUENCE 511 AA; 56563 MW; 7D3FAB4499836C9 CRC64;

Query Match 39.6%; Score 1103.5; DB 1; Length 511;
Best Local Similarity 43.1%; Pred. No. 4.3e-78;
Matches 227; Conservative 96; Mismatches 175; Indels 29; Gaps 9;

QY 8 QOKVCLVVDGWSLDEQHGNAIAKAKTIPMDKLCGNNWOK-----LEAHLGHVGLPEGL 62
DB 3 KKPVALIILDFALRDEKGNVTHAKPNDRF---WNEYPHATLOASAEVGLPEGO 58
QY 63 MGNSEVGHNLGTAGRIYQDVRINLAVQRNEFTNPQIVASAEKRAKGGRLHLLGLVS 122
DB 59 MGNSEVGHNLGTAGRIYQDVRINLAVQRNEFTNPQIVASAEKRAKGGRLHLLGLVS 118
QY 123 DGGVSHDHLFALIRAFKOLQVPKTHFFADGRDTPSPTSGAGYLQQLQFIASEKYE 182
DB 119 DGGVSHDHLFALIRAFKOLQVPKTHFFADGRDTPSPTSGAGYLQQLQFIASEKYE 178
QY 183 LATITGRYAMDRKRWERIKMAYEAIVGGIGOKATVDKAVDVVRYRVAQSETDEFLKP- 241
DB 179 IATISGRYAMDRKRWERIKMAYEAIVGGIGOKATVDKAVDVVRYRVAQSETDEFLKP- 236
QY 242 IVFSDDG-----RVKDDDTLTFNRYADRMROICELGLERYKLNSSVPHPKNTQISGMT 297
DB 237 VITREKDSGPVATIQEDAVIFNFRPDRAIQISNTEANEDFRSDRGEKPKHLHFVCLT 296
QY 298 QYNKEFPSPFLPPVTHNVLAELWASGVTFQFCAETEKYPHYTFFNGREVOFQDEE 357
DB 297 HFSEVTDGYVAFKPINLNDTLEVLSONNLKQLRAETEKYPHYTFFMSGGREAEPFGE 356
QY 358 RCWVSPKREKATYDLKPMNAAGVAEKVQIESGRHPLVNCNFPAPDMVGHGKFFPAV 417
DB 357 RILIDSPK-VATYDLKPMNAAGVAEKVQIESGRHPLVNCNFPAPDMVGHGKFFPAV 415
QY 418 KACQATDEAIGKIFACQYQYNYVLMVTSDHGNAEKMIAPDGSHTAHTCNLPVPTCSK 477
DB 416 KAIETVDECLGKIVDAILAKGTAITADHGNADDEVITLGNPMTHNTNVP-----V 469
QY 478 FVFKSTPTGDDGKERARALRDVAPTVLQL-MGLPVPVPMGVPLLE 523
DB 470 IVTKOGLLELREDG-----ILGDLAPTMLTLFLDVAQPKMTGKTLIK 511
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RESULT 11

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GPML_PSEAE
ID GPML_PSEAE STANDARD; PRT; 515 AA.
AC Q9HU53;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 2,3-bisphosphoglycerate-independent phosphoglycerate mutase
DE (EC 5.4.2.1) (Phosphoglyceromutase) (BPG-independent PGAM) (iPGM).
GN GPML OR PGM OR PA5131.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.A.
RC STRAIN=ATCC 15692 / PAOI;
RX MEDLINE=2043737; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
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RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RA "Complete genome sequence of Pseudomonas aeruginosa PAOI, an
RA opportunistic pathogen.";
RL Nature 406:959-964(2000).
CC -1- FUNCTION: Catalyzes the interconversion of 2-phosphoglycerate and
CC 3-phosphoglycerate (By similarity).
CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate -> 3-phospho-D-glycerate.
CC -1- COFACTOR: Binds 2 manganese ions (By similarity).
CC -1- PATHWAY: Glycolysis.
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: BELONGS TO THE BPG-INDEPENDENT PHOSPHOGLYCERATE MUTASE
CC FAMILY.
CC -----
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CC -----
DR EMBL; AE004926; AAC08516.1; -.
DR HAMAP; MF_01038; -.
DR InterPro; IPR006124; Metalloenzyme.
DR InterPro; IPR005995; Pgm_bpd_ind.
DR Pfam; PF01676; Metalloenzyme; 1.
DR ProDom; PD004429; Pgm_bpd_ind; 1.
DR TIGRFAMs; TIGR03307; Pgm_bpd_ind; 1.
KW Isomerase; Glycolysis; Metal-binding; Manganese; Complete proteome.
FT ACT_SITE 64 64
FT METAL 14 14 MANGANESE 2 (BY SIMILARITY).
FT METAL 64 64 MANGANESE 2 (BY SIMILARITY).
FT METAL 404 404 MANGANESE 1 (BY SIMILARITY).
FT METAL 408 408 MANGANESE 1 (BY SIMILARITY).
FT METAL 445 445 MANGANESE 2 (BY SIMILARITY).
FT METAL 446 446 MANGANESE 2 (BY SIMILARITY).
FT METAL 464 464 MANGANESE 1 (BY SIMILARITY).
SQ SEQUENCE 515 AA; 55601 MW; AC8C4404189BEC7 CRC64;

Query Match 39.1%; Score 1088.5; DB 1; Length 515;
Best Local Similarity 45.0%; Pred. No. 6.4e-77;
Matches 232; Conservative 78; Mismatches 180; Indels 25; Gaps 9;

QY 13 LWVIDGWLSDQHGNAIAKAKTIPMDKLCGNNWOKL-EAHLGHVGLPEGLMGNSEVGH 71
DB 10 LIIDGFGHSDPDYNAIYAAKPVMDRLLATQPHGLISGSGMDVGLPDGQMGSEVGH 69
QY 72 NIGAGRVYQDVRINLAVQRNEFTNPQIVASAEKRAKGGRLHLLGLVSDGGVHSHID 131
DB 70 NLGAGRVYQDVRINLAVQRNEFTNPQIVASAEKRAKGGRLHLLGLVSDGGVHSHID 129
QY 132 HLFALIRAFKOLQVPKTHFFADGRDTPSPTSGAGYLEQLQFIASEKYGELATIGRY 191
DB 130 HLVAQAQAARRAGKIVLHFLDGRDTPPKSAQPSLERLDATFAGLKGRIASITIGRY 189
QY 192 AMDRDKRWERIKMAYEAIVGGIGOKATVDKAVDVVRYRVAQSETDEFLKPIVSDDG--- 248
DB 190 AMDRDKRWERIKMAYEAIVGGIGOKATVDKAVDVVRYRVAQSETDEFLKPIVSDDG--- 248
QY 249 -RVKDDDTLTFNRYADRMROICELGLERYKLNSSVPHPKNTQISG---MTOYKNEFP 304
DB 249 VRVEDGDAVIFNFRPDRAIQISNTEANEDFRSDRGEKPKHLHFVCLTQAASIP 304
QY 305 PPSLFPVPTHTNVLAELWASGVTFQFCAETEKYPHYTFFNGREVOFQDEERWVSP 364
DB 305 APCAFPEPLTNVLGEYLAKHGKTKQLRAETEKYAHVTFPFGSGREEPEEERILLISP 364
QY 365 KEVATYDLKPMNAAGVAEKVQIESGRHPLVNCNFPAPDMVGHGKFFPAVKACQATD 424
DB 365 K-VATYDLQPEMSAPEVTDRIEATQEQRYDVIVVNVANGMDVGHGKFFPAVKACQATD 423
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QY 425 EAIGKIFEACQTYNYVLMVTSRHGNAEKM-IAPDGSSEHTAHTCNLVPFTCSSTFFKST 483
Db 424 TCMGRIVEALDKVGGEALITADHGNVEQMEDESTGOAHTAHTCEPVPF-----VYVGKRK 478
QY 484 PPTGDDGKERARALRDVAPTVLQMLGLPVPPEMDG 518
Db 479 LSIREGG-----VLADVAPTMLTLMGLEQPAEMTG 508

RESULT 12
GPML_VIBCH STANDARD; PRT; 510 AA.
AC Q9KV22;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 2,3-bisphosphoglycerate-independent phosphoglycerate mutase
DE (EC 5.4.2.1) (Phosphoglyceromutase) (BPG-independent PGAM) (IPGM).
GN GPML OR VC0336.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Emolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae."
RL Nature 406:477-483(2000).
CC -1- FUNCTION: Catalyzes the interconversion of 2-phosphoglycerate and
CC 3-phosphoglycerate (By similarity).
CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = 3-phospho-D-glycerate.
CC -1- COFACTOR: Binds 2 manganese ions (By similarity).
CC -1- PATHWAY: Glycolysis.
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: BELONGS TO THE BPG-INDEPENDENT PHOSPHOGLYCERATE MUTASE
CC FAMILY.
CC -----
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CC -----
DR EMBL; AE004122; AAF93509.1;
DR PIR; G82335; G82335.
DR TIGR; VC0336;
DR HAMAP; MF 01038; 1.
DR InterPro; IPR006124; Metalloenzyme.
DR InterPro; IPR005995; pgm_bpd_ind.
DR Pfam; PF01676; Metalloenzyme; 1.
DR ProDom; PD004429; pgm_bpd_ind; 1.
DR TIGRfam; TIGR01307; pgm_bpd_ind; 1.
KW Isomerase; Glycolysis; Metal-binding; Manganese; Complete proteome.
FT ACT_SITE 63 63 PHOSPHOSERINE INTERMEDIATE
FT METAL 13 13 (BY SIMILARITY).
FT METAL 63 63 MANGANESE 2 (BY SIMILARITY).
FT METAL 401 401 MANGANESE 1 (BY SIMILARITY).
FT METAL 405 405 MANGANESE 1 (BY SIMILARITY).
FT METAL 442 442 MANGANESE 2 (BY SIMILARITY).
FT METAL 443 443 MANGANESE 2 (BY SIMILARITY).
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FT METAL 461 461 MANGANESE 1 (BY SIMILARITY).
SQ SEQUENCE 510 AA; 55364 MW; 0607A64DA6DD955B CRC64;
Query Match 38.9%; Score 1083.5; DB 1; Length 510;
Best Local Similarity 43.1%; Pred. No. 1.5e-76;
Matches 226; Conservative 87; Mismatches 180; Indels 31; Gaps 10;
QY 6 NVQOKVCLVVIDGWSLSDQHGNAIAKARTPMDKILCSGNWOKL-BAHGLHVLGPLEGLMG 64
Db 2 SAKKPMALVLDGWGYREDNANNAINNARTPVMDSLMANNPHTLISASGMDVGLPDQMG 61
QY 65 NSEVGHNLNAGRVIVQDIVRINLAVORNEFVTVNPOIVASAEKAGSRHLHLGLVSDG 124
Db 62 NSEVGHNLNAGRVIVQDIVRINLAVORNEFVTVNPOIVASAEKAGSRHLHLGLVSDG 121
QY 125 GVHSHIDLHALIRAFKQLQVQKVFIFHFFADGRTDTSPTSCAGVLEQLQLFIASEKYGELA 184
Db 122 GVHSHEDHIYAAVEMAAARGAEKIYLHCLFDGRDTPPSAEASLKRFDLFAKLKGRIA 181
QY 185 TITGRYAMDRDRKWERIKWAYEAIYVGGIGQKATVDKAVDVVRERYAQSETDEFLKPIVF 244
Db 182 SIVGRYAMDRDNMDRVEKAYDLLTLAQGE-FTYDSAVEALQAAVARENDEFVKATEI 240
QY 245 SDDGR-----VKDDDTLIFNYRADRMQIC-----ECLGLERYKDLNNSVPHPKNTQISG 295
Db 241 RAAGQESAAMQDGDALLFMNRYRADRARQITRTFVPDFAGFSR-----KAPP-----ALDFVM 292
QY 296 MTQYNKEFPFPIPEVTHNTVLAELASQGVTOFHCAETEKYPHVTFEFGNGREVQFOD 355
Db 293 LTQYAADIPLOCAFGPASLENTYGEWLSKAGTKQLRISETEKIAHYHTFFNGVENEFP 352
QY 356 EERCWVPSKEVATYDLKPEMNAAGVAERKVVQIESGRHPLVMCNCFAPDPDWGHTGKFE 415
Db 353 EERQLVASPK-VATYDLQPEMSSKELTDKLVAAIKSGKYDAIICNYPNGMDVGHGTGYEA 411
QY 416 AVKACQATDEATGKIFEACQTYNYVLMVTSRHGNAEKMIAPD-GSHTAHTCNLVPFTCS 474
Db 412 AVKACEAVDECIGRVVEAIKEVDGQLLITADHGNAEEMMIDPETGGVHTAHTSLPVL--- 468
QY 475 SKTFYFKSPPTGDDGKERARALRDVAPTVLQMLGLPVPPEMDG 518
Db 469 --IYGVNKAISLKEGK-----LSDLAPTMLALSOLDIPADMSG 505

RESULT 13
GPML_SALTI STANDARD; PRT; 514 AA.
AC Q822F0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE 2,3-bisphosphoglycerate-independent phosphoglycerate mutase
DE (EC 5.4.2.1) (Phosphoglyceromutase) (BPG-independent PGAM) (IPGM).
GN GPML OR STY4091 OR T3815.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21533947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connerion P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Felwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Whitehead S., Barrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18."
RL Nature 413:848-852(2001).
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RN  [2]
RC  SEQUENCE FROM N.A.
RP  STRAIN=Ty2 / ATCC 700931;
RX  MEDLINE=12531367; PubMed=12644504;
RA  Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA  Burland V., Kodyouranni V., Schwartz D.C., Blattner F.R.;
RT  "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT  and Cr18."
RL  J. Bacteriol. 185:2330-2337(2003).
CC  -1- FUNCTION: Catalyzes the interconversion of 2-phosphoglycerate and
CC  3-phosphoglycerate (By similarity).
CC  -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = 3-phospho-D-glycerate.
CC  -1- COFACTOR: Binds 2 manganese ions (By similarity).
CC  -1- PATHWAY: Glycolysis.
CC  -1- SUBUNIT: Monomer (By similarity).
CC  -1- SIMILARITY: BELONGS TO THE BPG-INDEPENDENT PHOSPHOGLYCERATE MUTASE
CC  FAMILY.
CC  -----
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CC  -----
DR  EMBL; AL627280; CAD03290.1; ALT_INIT.
DR  EMBL; AE016847; AA071297.1; ALT_INIT.
DR  HAMAP; MF_01038; -. 1.
DR  InterPro; IPR006124; Metalloenzyme.
DR  InterPro; IPR005995; Pgm_bpd_ind.
DR  Pfam; PF01676; Metalloenzyme; 1.
DR  ProDom; PD004429; Pgm_bpd_ind; 1.
DR  TIGRFAMs; TIGR01307; Pgm_bpd_ind; 1.
KW  Isomerase; Glycolysis; Metal-binding; Manganese; Complete proteome.
FT  ACT_SITE 64
FT  ACT_SITE 64
FT  METAL 14
FT  METAL 64
FT  METAL 64
FT  METAL 403
FT  METAL 407
FT  METAL 407
FT  METAL 444
FT  METAL 445
FT  METAL 463
FT  METAL 463
SQ  SEQUENCE 514 AA; 56312 MW; 48E8D203AABE3D34 CRC64;

Query Match 38.8%; Score 1082; DB 1; Length 514;
Best Local Similarity 42.1%; Pred. No. 2e-76;
Matches 223; Conservative 96; Mismatches 171; Indels 40; Gaps 10;

QY 8 QOKVCLVVDGWLSDQHGNAIAKATPIMDKLCSGNWOK-----LEAHGLHVLPEGL 62
DB 5 KKPWLVILDGGRYEEQDQDAINAKTPVMDAL-----WAKRPTLIDASGLEVLGPDQ 60
QY 63 MGNEVGHNLGAGRIYQDTRINLAVQRNEFTVNTQIVASAEKAKGSGRLHLGLVS 122
DB 61 MGNEVGHNLGAGRIYQDTRLDLVEIKERTFEANPVLTVNAVQAKNAGRAVHMGLLS 120
QY 123 DGGVHSHDHLFALIRAFKQLQVVFHFFADGRDTSPTSGAGYLEQLLOFIASEKYE 182
DB 121 AGGVHSHEDHTVMAELAAERGAEKIYILHAFLDGRDTPPRSAEASLKKFKDFAALGKR 180
QY 183 LATITGRYYAMDRKWRERIKWAYEIVGGIGOKATVDKVDVVRERYAQSDEEFLKPI 242
DB 181 VASIVGRYYAMDRNRWRDVEKAYDLMTLAGOE-FQADTAVAGQAAYARDENDEFFVKAT 239
QY 243 VFSDGR-----VKDDDTLIFENYRADRMROI CECL-----GLERYKDLNLSVPHPKNIQ 292
DB 240 VIRAEQQAADAMGSDTLIFNFRADRAREITRAFVNADFDGFAKKVV-----NLN 291
QY 293 ISGMTQYNKEPPFPPLPPVTHVNLAEWLASQGVTFPHCAETKYPHVTFFFNGGREVQ 352
DB 292 FVMLTEAADIKTAVAYPPASLANFTGEWMAKNDKTLQRISETEKYAHVTFFFNGGVEEP 351

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QY 353 FQDERCMVSPKEVATYDLKPEMNAAGVAEKVQEIESGRHPLVMCMNEAPPDMVGHGK 412
DB 352 FAGEERILINSPK-VATYDLPQEMSSAELEKLVAAIESGYDTTIDTTPNGDMVGHGTV 410
QY 413 FEPAVKACQATDEAIGKIFACQTYNTVLMVTSDHGNAEKIAP-DGSEHTAHTCNLVPE 471
DB 411 MEAAIKAVEALDNCIEQTVAVESVGGQLLITADHGNAEQMRDPATGQHTAHTNLPVPL 470
QY 472 TCSKSTVFFKSTPTPTGDDGKERARALRDVAPTVLQMLGLPVPPMDGVPL 521
DB 471 -----IYVGEKNVKAVEGK-----LSDIAPTMLSLMGMEIPEQMTKPL 510

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RESULT 14

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GPML_ANASP
ID GPML_ANASP STANDARD; PRT; 533 AA.
AC OBYPL2;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 2,3-bisphosphoglycerate-independent phosphoglycerate mutase
DE (EC 5.4.2.1) (Phosphoglyceromutase) (bpg-independent PGAM) (iPGM).
GN GPML OR ALL4182.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriquchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120."
RL DNA Res. 8:205-213(2001).
CC -1- FUNCTION: Catalyzes the interconversion of 2-phosphoglycerate and
CC 3-phosphoglycerate (By similarity).
CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = 3-phospho-D-glycerate.
CC -1- COFACTOR: Binds 2 manganese ions (By similarity).
CC -1- PATHWAY: Glycolysis.
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: BELONGS TO THE BPG-INDEPENDENT PHOSPHOGLYCERATE MUTASE
CC FAMILY.
CC -----
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CC -----
DR PIR; AG2328; AG2328.
DR HAMAP; MF_01038; 1.
DR InterPro; IPR006124; Metalloenzyme.
DR InterPro; IPR005995; Pgm_bpd_ind.
DR Pfam; PF01676; Metalloenzyme; 1.
DR ProDom; PD004429; Pgm_bpd_ind; 1.
DR TIGRFAMs; TIGR01307; Pgm_bpd_ind; 1.
KW Isomerase; Glycolysis; Metal-binding; Manganese; Complete proteome.
FT ACT_SITE 65
FT ACT_SITE 65
FT METAL 15
FT METAL 65
FT METAL 65
FT METAL 398
FT METAL 402
FT METAL 402
FT METAL 439
FT METAL 440
FT METAL 440
FT METAL 457

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SQ SEQUENCE 533 AA; 57677 MW; ACC40C19F612AF7C CRC64;
Query Match 38.7%; Score 1078; DB 1; Length 533;
Best Local Similarity 42.9%; Pred. No. 4.4e-76;
Matches 227; Conservative 85; Mismatches 179; Indels 38; Gaps 10;

QY 11 VCLVVDGWSLDEQHGNAIAKAKTIPMDKLCGNNQK-----LEAGHLHVLPEGLMGN 65
DQ 9 VLVVLDGWSLDEQHGNAIAKAKTIPMDKLCGNNQK-----LEAGHLHVLPEGLMGN 64
QY 66 SEVGHNLNAGRIYODIVRINLAVORNEFVNPQIVASAEKAKKSGRHLHGLVSDGG 125
DQ 65 SEVGHNLNAGRIYODIVRINLAVORNEFVNPQIVASAEKAKKSGRHLHGLVSDGG 124
QY 126 VHSIDHFLALIRAFKQLQVVKVFIHFFADGRDTSPTSGAGYLEQLLQFTASEKYCELAT 185
DQ 125 VHSIDHFLALIRAFKQLQVVKVFIHFFADGRDTSPTSGAGYLEQLLQFTASEKYCELAT 184
QY 186 ITGRYYAMDRDRKWRERIKMAYEIV-GGIGQKATVDKAVDVVRERYAQSETDFLKPIVE 244
DQ 185 VSGRYAMDRDRKWRERIKMAYEIV-GGIGQKATVDKAVDVVRERYAQSETDFLKPIVE 241
QY 245 SDGRYKDDTLFFNYRADRMQIC-----ECIGLERYKDLNLSVPPKNIQISGMQ 298
DQ 242 A-PGTVEPQGVIFNFRDRSRQLQAFVSPFTGFARQQ-----IKPLSFVTFQ 292
QY 299 YNKEFPFSLFPVTHNTNVLAEWLASQGVTFQFHAETEKYPHVTFFNGGREGVQFDEER 358
DQ 293 YDSLSVSAFEPQNLNLGEVIANQGLNQFTAEKTAHYTFYFNGGLEPFAGEDR 352
QY 359 CMVPSPEKATVDLKPENMAAGVAEKVPOIESGRHPLVNCNFPAPDPMDVGHGTGKFPAYK 418
DQ 353 ELVSSPM-VATYDKAPAMSAVATDTAIAAQGIYSLIVINYPANPMDVGHGTGKFPAYK 411
QY 419 ACQATDEATGKIFEACQTYNYVLMVTDHGNNAEKMTAPDSEHTATCNLYPFTCSKTF 478
DQ 412 ALETVDRCILLEGVSKAGGTITITADHGNNAEKMTAPDSEHTATCNLYPFTCSKTF 471
QY 479 V-----FKSTPTGDDGKERARALRDVAPTVLQMLGLVPPEMDGVPLLE 523
DQ 472 VKIPGYGTNVELRSDGK-----LADIATPILDIQLPQPEMTGRSLIQ 515

RESULT 15
GPMI_SALTY STANDARD; PRT; 514 AA.
AC Q8ZL56;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 2,3-bisphosphoglycerate-independent phosphoglycerate mutase
DE (EC 5.4.2.1) (Phosphoglyceromutase) (BPG-independent PGAM) (IPGM).
GN GPMI OR PMGI OR STM3704.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leon E., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RL Nature 413:852-856(2001).
CC -1- FUNCTION: Catalyzes the interconversion of 2-phosphoglycerate and
CC 3-phosphoglycerate (By similarity).
CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate -> 3-phospho-D-glycerate.
CC -1- COFACTOR: Binds 2 manganese ions (By similarity).
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